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Assistant Professor

Computer Science and Software Engineering
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Research Interests

- Bioinformatics and Computational Biology
- Machine Learning and Data Mining
- Data Science and Big Data Analytics

Faculty Positions

Assistant Professor 2017 – Present
Department of Computer Science and Software Engineering
Auburn University

Assistant Professor 2016 – 2017
Department of Electrical Engineering and Computer Science
Wichita State University

Education

Ph.D. in Computer Science 2016
University of Missouri – Columbia

M.S. in Computer Science 2014
University of Missouri – Columbia

B.Tech. in Computer Science and Engineering 2005
Haldia Institute of Technology, India

Research Accomplishments

- Lead developer of one of the 19 most innovative methods worldwide in CASP11, 2014.
- Lead author of the top 10 most cited and the most accessed article in Proteins, 2013.
- Lead developer of the No.1 protein refinement server worldwide in CASP10, 2012.

Professional Memberships

- International Society for Computational Biology (ISCB)
- Association for Computing Machinery (ACM)
- Institute of Electrical and Electronics Engineers (IEEE)

Publications

Journals:

12. D. Bhattacharya, R. Cao, J. Cheng. "UniCon3D: de novo protein structure prediction using united-residue conformational search via stepwise, probabilistic sampling". *Bioinformatics*, 32 (18): 2791-2799 (2016).
11. D. Bhattacharya, J. Nowotny, R. Cao, J. Cheng. "3Drefine: An Interactive Web Server for Efficient Protein Structure Refinement". *Nucleic Acids Research, Web Server Issue*, 4 (W1): W406-W409 (2016).
10. R. Cao, B. Adhikari, D. Bhattacharya, M. Sun, J. Hou, J. Cheng. "QAcon: single model quality assessment using protein structural and contact information with machine learning techniques". *Bioinformatics*, 33 (4): 586-588 (2017).
9. D. Bhattacharya, B. Adhikari, J. Li, J. Cheng. "FRAGSION: ultra-fast protein fragment library generation by IOHMM sampling". *Bioinformatics*, 32 (13): 2059-2061 (2016).
8. R. Cao, D. Bhattacharya, J. Hou, J. Cheng. "DeepQA: improving the estimation of single protein model quality with deep belief networks". *BMC Bioinformatics*, 17: 495 (2016).
7. B. Adhikari, J. Nowotny, D. Bhattacharya, J. Hou, J. Cheng. "ConEVA: a Toolbox for Comprehensive Assessment of Protein Contacts". *BMC Bioinformatics*, 17: 517 (2016).
6. D. Bhattacharya, J. Cheng. "De novo protein conformational sampling using a probabilistic graphical model". *Nature Scientific Reports*, 5: 16332 (2015).
5. R. Cao, D. Bhattacharya, B. Adhikari, J. Li, J. Cheng. "Massive integration of diverse protein quality assessment methods to improve template based modeling in CASP11". *Proteins*, 84(S1): 247-259 (2015).
4. B. Adhikari, D. Bhattacharya, R. Cao, J. Cheng. "CONFOLD: Residue-residue contact guided ab initio protein folding". *Proteins*, 83(8): 1436-1449 (2015).
3. R. Cao, D. Bhattacharya, B. Adhikari, J. Li, J. Cheng. "Large-scale model quality assessment for improving protein tertiary structure prediction". *Bioinformatics*, 31(12): i116-i123 (2015).
2. D. Bhattacharya, J. Cheng. "i3Drefine software for protein 3D structure refinement and its assessment in CASP10". *PLOS ONE*, 8(7): e69648 (2013).
1. D. Bhattacharya, J. Cheng. "3Drefine: Consistent Protein Structure Refinement by Optimizing Hydrogen Bonding Network and Atomic Level Energy Minimization". *Proteins*, 81(1): 119-131 (2013).

Conferences:

3. R. Cao, D. Bhattacharya, B. Adhikari, J. Li, J. Cheng. "Large-scale model quality assessment for improving protein tertiary structure prediction". *ISMB*. (2015).
2. D. Bhattacharya, J. Cheng. "Protein Structure Refinement by Iterative Fragment Exchange". *ACM-BCB*. (2013).
1. B. Adhikari, X. Deng, J. Li, D. Bhattacharya, J. Cheng. "A Contact-Assisted Approach to Protein Structure Prediction and Its Assessment in CASP10". *AAAI*. (2013).

Book Chapters:

2. B. Adhikari, D. Bhattacharya, R. Cao, J. Cheng. "Assessing Predicted Contacts for Building Protein Three-Dimensional Models". *Springer*, 1484: 115-126 (2017).
1. J. Li, D. Bhattacharya, R. Cao, B. Adhikari, X. Deng, J. Eickholt, J. Cheng. "The MULTICOM Protein Tertiary Structure Prediction System". *Springer*, 1137: 29-41 (2013).